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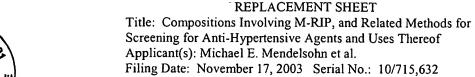


Fig0/6 GE	e 1A : 1 of 2		
Humar		MSAAKENPCRKFQANIFNKSKCQNCFKPREPHLLNDEDLTQAKPIYGGWLLLAPDGTDFD	60
Mouse	e: 1	MSAAKENPCRKFQANIFNKSKCQNCFKPRE HLLNDEDLTQAKPIYGGWLLLAPDGTDFD MSAAKENPCRKFQANIFNKSKCQNCFKPRESHLLNDEDLTQAKPIYGGWLLLAPDGTDFD	60
Humar	n: 61	NPVHRSRKWQRRFFILYEHGLLRYALDEMPTTLPQGTINMNQCTDVVDGEGRTGQKFSLC NPVHRSRKWQRRFFILYEHGLLRYALDEMPTTLPQGTINMNQCTDVVDGE RTGQKFSLC	120
Mouse	e: 61	NPVHRSRKWQRRFFILYEHGLLRYALDEMPTTLPQGTINMNQCTDVVDGEARTGQKFSLC	120
Humar	n: 121	ILTPEKEHFIRAETKEIVSGWLEMLMVYPRTNKQNQKKKRKVEPPTPQEPGPAKVAVTSS ILTP+KEHFIRAETKEI+SGWLEMLMVYPRTNKQNQKKKRKVEPPTPQEPGPAK+AVTSS	180
Mouse	e: 121	ILTPDKEHFIRAETKEIISGWLEMLMVYPRTNKQNQKKKRKVEPPTPQEPGPAKMAVTSS	180
Human	n: 181	SSSSSSSSIPSAEKVPTTKSTLWQEEMRTKDQPDGSSLSPAQSPSQSQPPAASSLREP S +S SSSSIPSAEKVPTTKSTLWQEEMR KDQPDG+SLSPAQSPSQSQPPAA + REP	238
Mouse	e: 181	SGGTSGSSSSIPSAEKVPTTKSTLWQEEMRAKDQPDGTSLSPAQSPSQSQPPAACTPREP	240
Human	n: 239	GLESKEEESAMSSDRMDCGRKVRVESGYFSLEKTKQDLKAEEQQLPPPLSPPSPSTPNHR GLESKE+ES +S DR+D GRKVRVESGYFSLEK KQDL+AEEQ LPP LSPPSPSTP+ R	298
Mouse	e: 241	GLESKEDESTISGDRVDGGRKVRVESGYFSLEKAKQDLRAEEQ-LPPLLSPPSPSTPHSR	299
Human	n: 299	RSQVIEKFEALDIEKAEHMETNA-VGPSPSSDTRQGRSEKRAFPRKRDFTNEAPPAPLPD RSQVIEKFEALDIEKAEHMETN + +PSSDTRQGRSE+RA PRKRDF +EAP APL D	357
Mouse	e: 300	RSQVIEKFEALDIEKAEHMETNMLILTTPSSDTRQGRSERRAIPRKRDFASEAPTAPLSD	359
Human	1: 358	ASASPLSPHRRAKSLDRRSTEPSVTPDLLNFKKGWLTKQYEDGQWKKHWFVLADQSLRYY A PLSPHRRAKSLDRRSTE S+TPDLLNFKKGWLTKQYEDGQWKKHWFVLADQSLRYY	417
Mouse	e: 360	ACPLSPHRRAKSLDRRSTESSMTPDLLNFKKGWLTKQYEDGQWKKHWFVLADQSLRYY	417
Human	n: 418	RDSVAEEAADLDGEIDLSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI RDSVAEEAADLDGEI+LS CYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI	477
Mouse	e: 418	RDSVAEEAADLDGEINLSTCYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI	477
Human	1: 478	MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKQEAELGEPDPEQKTSRARERRREG MKHV P +APDVTSSLPE KNKS+ SFETC R TEKQEAE GEPDPEQK SRARERRREG	537
Mouse	: 478	MKHVLPASAPDVTSSLPEGKNKST-SFETCSRSTEKQEAEPGEPDPEQKKSRARERRREG	536
Human	1: 538	RSKTFDWAEFRPIQQALAQERVGGVGPADTHEPLRPEAESGELERERARREERRKRFGM RSKTFDWAEFRPIQQALAQER VG +D+ +P EAE GELERERARREE RKRFGM	597
Mouse	e: 537	RSKTFDWAEFRPIQQALAQERASAVGSSDSGDPGCLEAEPGELERERARREEPRKRFGM	
Human	ı: 598	LDATDGPGTEDAALRMEVDRSPGL-PMSDLKTHNVHVEIEQRWHQVETTPLREEKQVPIA LD DGPG ED ALRM++DRSPGL DLKT NVHVEIEQRWHQVETTPLREEKQVPIA	
	: 597	LDTIDGPGMEDTALRMDIDRSPGLLGTPDLKTQNVHVEIEQRWHQVETTPLREEKQVPIA	
	ı: 657	PVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQNRLLQDQLRVALGREQSAREG P+HLS ED +RLSTHELTSLLEKELEQSQKEASDLLEQNRLLQDQLRVALGREQSAREG	716
Mouse	: 657	PLHLSLEDRSERLSTHELTSLLEKELEQSQKEASDLLEQNRLLQDQLRVALGREQSAREG	716
Human	ı: 717	YVLQATCERGFAAMEETHQKKIEDLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKN YVLQATCERGFAAMEETHQKKIEDLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKN	
Mouse	: 717	YVLQATCERGFAAMEETHQKKIEDLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKN	776
Human	ı: 777	AHREEMERELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSEQYSQKCLENAHL AHREEMERELEKSQRSQISS+NSD+EALRRQYLEELQSVQRELEVLSEQYSQKCLENAHL	
Mouse	: 777	AHREEMERELEKSQRSQISSINSDIEALRRQYLEELQSVQRELEVLSEQYSQKCLENAHL	836

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Figure 1A PAGE 2 of 2

Human: 837 AQALEAERQALRQCQRENQELNAHNQELNNRLAAEITRLRTLLTGDGGGEATGSPLAQGK 896

AQALEAERQALRQCQRENQELNAHNQELNNRLAAEITRLRTLLTGDGGGE+TG PL QGK

Mouse: 837 AQALEAERQALRQCQRENQELNAHNQELNNRLAAEITRLRTLLTGDGGGESTGLPLTQGK 896

Human: 897 DAYELEVLLRVKESEIQYLKQEISSLKDELQTALRDKKYASDKYKDIYTELSIAKAKADC 956

DAYELEVLLRVKESEIQYLKQEISSLKDELQTALRDKKYASDKYKDIYTELSIAKAKADC 956

Mouse: 897 DAYELEVLLRVKESEIQYLKQEISSLKDELQTALRDKKYASDKYKDIYTELSIAKAKADC 956

Human: 957 DISRLKEQLKAATEALGEKSPDSATVSGYDIMKSKSNPDFLKKDRSCVTRQLRNIRSKSV 1016

DISRLKEQLKAATEALGEKSP+ TVSGYDIMKSKSNPDFLKKDRSCVTRQLRNIRSKSV 1016

Human: 1017 IEQVSWDT 1024

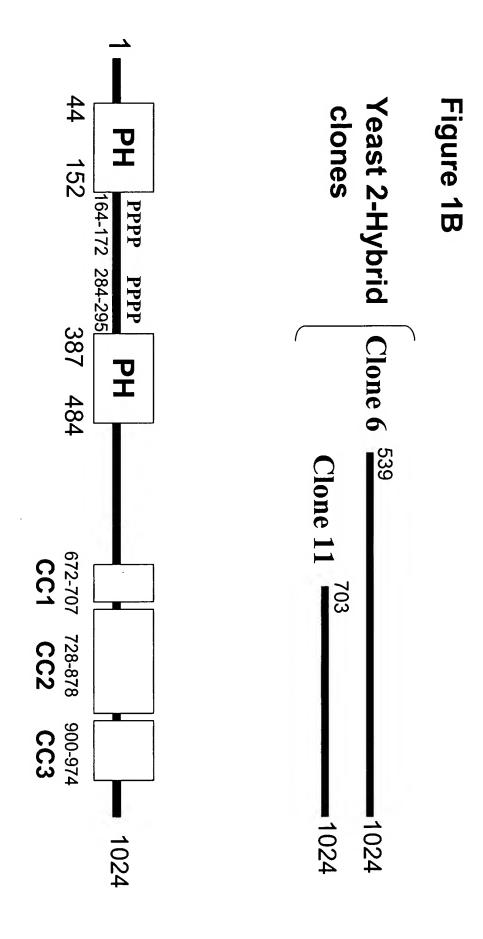
**IEQVSWD** 

Mouse: 1017 IEQVSWDN 1024

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### FIGURE 1C

SEQ ID NO: 19

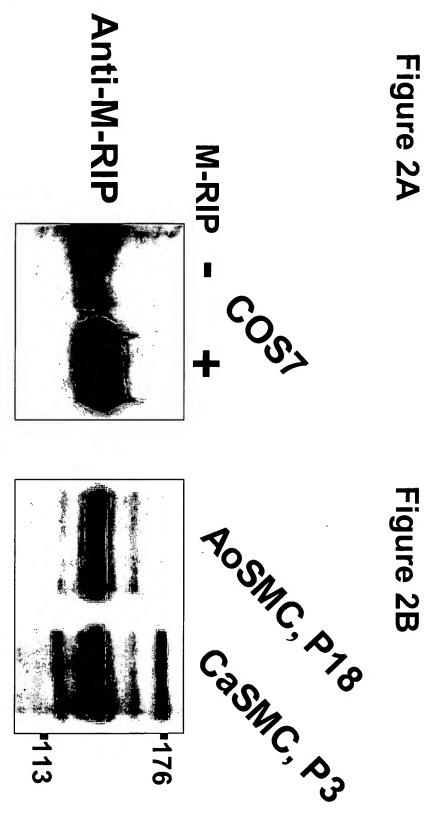
ATGTCGGCAGCCAAGGAAACCCGTGCAGGAAATTCCAGGCCAACATCTTCAACAAGAGCAAGTGTCAG AACTGCTTCAAGCCCCGCGAGCCGCATCTGCTCAACGACGAGGACCTGACGCAGGCAAAACCCATTTAT GGCGGTTGGCTCCTGGCTCCAGATGGGACCGACTTTGACAACCCAGTGCACCGGTCTCGGAAATGG CAGCGACGGTTCTTCATCCTTTACGAGCACGGCCTCTTGCGCTACGCCCTGGATGAGATGCCCACGACC CTTCCTCAGGGCACCATCAACATGAACCAGTGCACAGATGTGGTGGATGGGGAGGGCCGCACGGGCCAG AAGTTCTCCCTGTGTATTCTGACGCCTGAGAAGGAGCATTTCATCCGGGCGGAGACCAAGGAGATCGTC AGTGGGTGGCTGGAGATGCTCATGGTCTATCCCCGGACCAACAAGCAGAATCAGAAGAAGAAACGGAAA GTGGAGCCCCCACACCACAGGAGCCTGGGCCTGCCAAGGTGGCTGTTACCAGCAGCAGCAGCAGCAGCAGC AGCAGCAGCACCACCAGTGCTGAGAAAGTCCCCACCACCAAGTCCACACTCTGGCAGGAAGAAATG ATGGACTGTGGCCGCAAAGTCCGGGTGGAGAGCGGCTACTTCTCTCTGGAGAAGACCAAACAGGACTTG AAGGCTGAAGAACAGCAGCTGCCCCGCCGCTCTCCCCTCCCAGCCCCAGCACCCCCAACCACAGGAGG TCCCAGGTGATTGAAAAGTTTGAGGCCTTGGACATTGAGAAGGCAGAGCACATGGAGACCAATGCAGTG GGGCCCTCACCATCCAGCGACACACGCCAGGGCCGCAGCGAGAAGAGGGGCGTTCCCTAGGAAGCGGGAC TTCACCAATGAAGCCCCCCCAGCTCCTCTCCCAGACGCCTCGGCTTCCCCCCTGTCTCCACACCGAAGA GCCAAGTCACTGGACAGGAGGTCCACGGAGCCCTCCGTGACGCCCGACCTGCTGAATTTCAAGAAAGGC TGGCTGACTAAGCAGTATGAGGACGGCCAGTGGAAGAAACACTGGTTTGTCCTCGCCGATCAAAGCCTG ACCCTGTCGGCCATGACATCTGGGATTCGGCGGAACTGGATCCAGACCATCATGAAGCACGTGCACCCG ACCACTGCCCGGATGTGACCAGCTCGTTGCCAGAGGAAAAAAACAAGAGCAGCTGCTCTTTTGAGACC TGCCCGAGGCCTACTGAGAAGCAAGAGGCAGAGCTGGGGGAGCCGGACCCTGAGCAGAAGACGAGCCGC GCACGGGAGCGGAGGCGAGAGGCCGCTCCAAGACCTTTGACTGGGCTGAGTTCCGTCCCATCCAGCAG GCCCTGGCTCAGGAGCGGGTGGGCGTGGGGCCTGCTGACACCCACGAGCCCCTGCGCCCTGAGGCC GACGCCACAGACGGGCCAGGCACTGAGGATGCAGCCCTGCGCATGGAGGTGGACCGGAGCCCAGGGCTG CCTATGAGCGACCTCAAAACGCATAACGTCCACGTGGAGATTGAGCAGCGGTGGCATCAGGTGGAGACC ACACCTCTCCGGGAAGAAGCAGGTGCCCATCGCCCCCGTCCACCTGTCTTCTGAAGATGGGGGTGAC CGGCTCTCCACACACGAGCTGACCTCTCTGCTCGAGAAGGAGCTGGAGCAGAGCCAGAAGGAGGCCTCA GACCTTCTGGAGCAGAACCGGCTCCTGCAGGACCAGCTGAGGGTGGCCCTGGGCCGGGAGCAGAGCGCC CGTGAGGGCTACGTGCAGGCCACGTGCGAGCGAGGGTTTGCAGCAATGGAAGAAACGCACCAGAAG AAGATTGAAGATCTCCAGAGGCAGCACCAGCGGGAGCTAGAGAAACTTCGAGAAGAGAAAAAGACCGCCTC CTAGCCGAGGAGACAGCGGCCACCATCTCAGCCATCGAAGCCATGAAGAACGCCCACCGGGAGGAAATG GAGCGGGAGCTGGAGAAGAGCCAGCGGTCCCAGATCAGCAGCGTCAACTCGGATGTTGAGGCCCTGCGG CGCCAGTACCTGGAGGAGCTGCAGTCGGTGCAGCGGGAACTGGAGGTCCTCTCGGAGCAGTACTCGCAG AAGTGCCTGGAGAATGCCCATCTGGCCCAGGCGCTGGAGGCCGAGCGGCAGGCCCTGCGGCAGTGCCAG CGTGAGAACCAGGAGCTCAATGCCCACAACCAGGAGCTGAACAACCGCCTGGCTGCAGAGATCACACGG TTGCGGACGCTGCTGACTGGGGACGCGGTGGGGAGGCCACTGGGTCACCCCTTGCACAGGGCAAGGAT GCCTATGAACTAGAGGTCTTATTGCGGGTAAAGGAATCGGAAATACAGTACCTGAAACAGGAGATTAGC TCCCTCAAGGATGAGCTGCAGACGGCACTGCGGGACAAGAAGTACGCAAGTGACAAGTACAAAGACATC TACACAGAGCTCAGCATCGCGAAGGCTAAGGCTGACTGTGACATCAGCAGGTTGAAGGAGCAGCTCAAG GCTGCAACGGAAGCACTGGGGGAGAAGTCCCCTGACAGTGCCACGGTGTCCGGATATGATAATGAAA TCTAAAAGCAACCCTGACTTCTTGAAGAAAGACAGATCCTGTGTCACCCGGCAACTCAGAAACATCAGG TCCAAGTCCGTAATTGAGCAGGTCTCGTGGGATACCTGA



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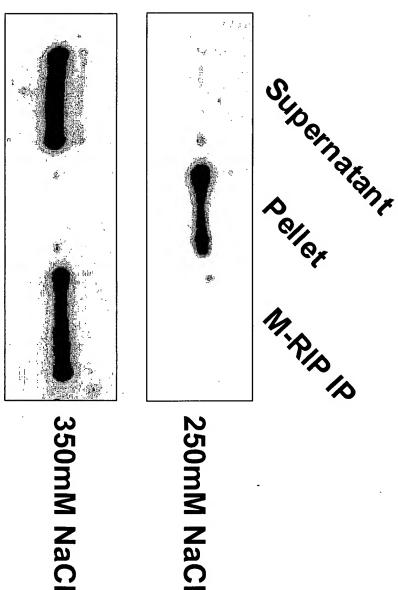


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250mM NaCl

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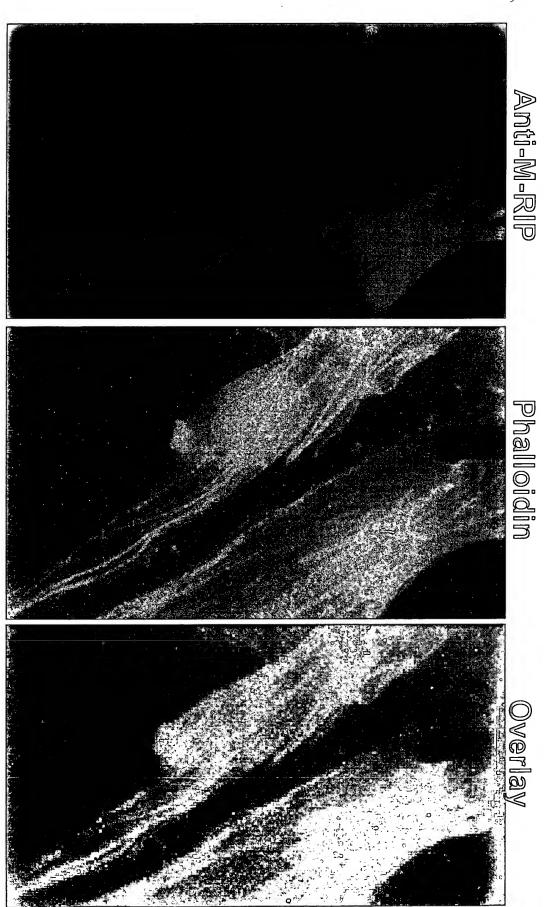


Figure 2D

Title: Compositions Involving M-RIP, and Related Methods for Screening for Anti-Hypertensive Agents and Uses Thereof

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## Figure 3A Anti-M-RIP **Anti-MBS** Soo Indus Noninnmune log Naple In Market In Ma

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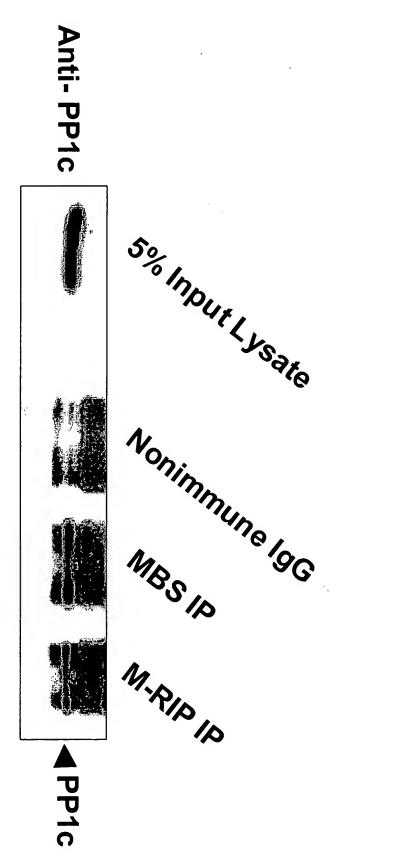
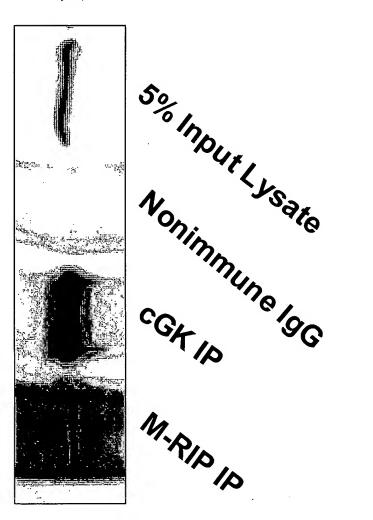


Figure 3B

Title: Compositions Involving M-RIP, and Related Methods for Screening for Anti-Hypertensive Agents and Uses Thereof

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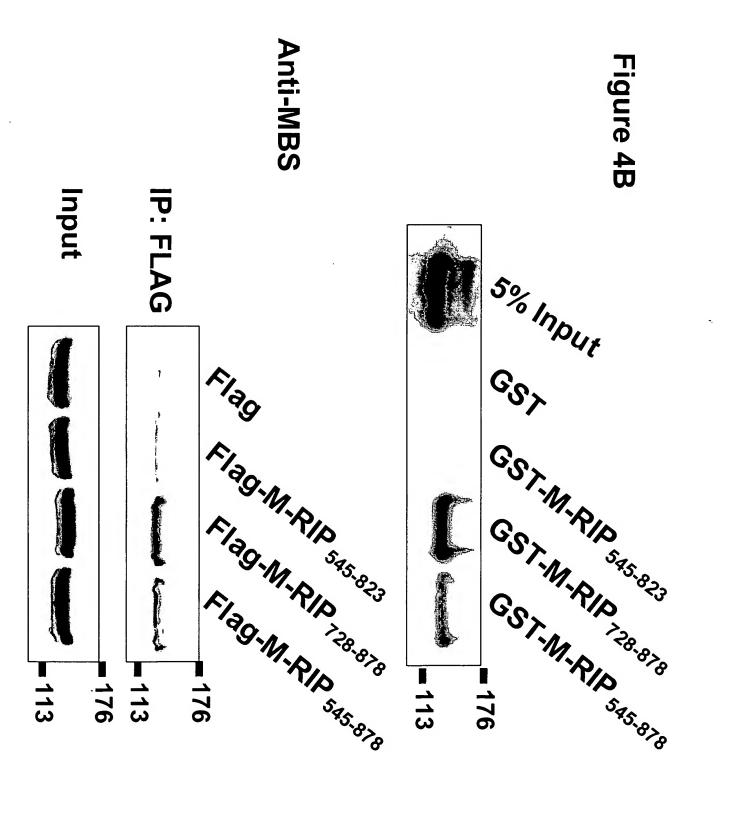
# **Anti-MBS** S% Input GST.CCT GST.CCT GST.CC3 GST.CGA 1.50

Figure 4A

Title: Compositions Involving M-RIP, and Related Methods for Screening for Anti-Hypertensive Agents and Uses Thereof

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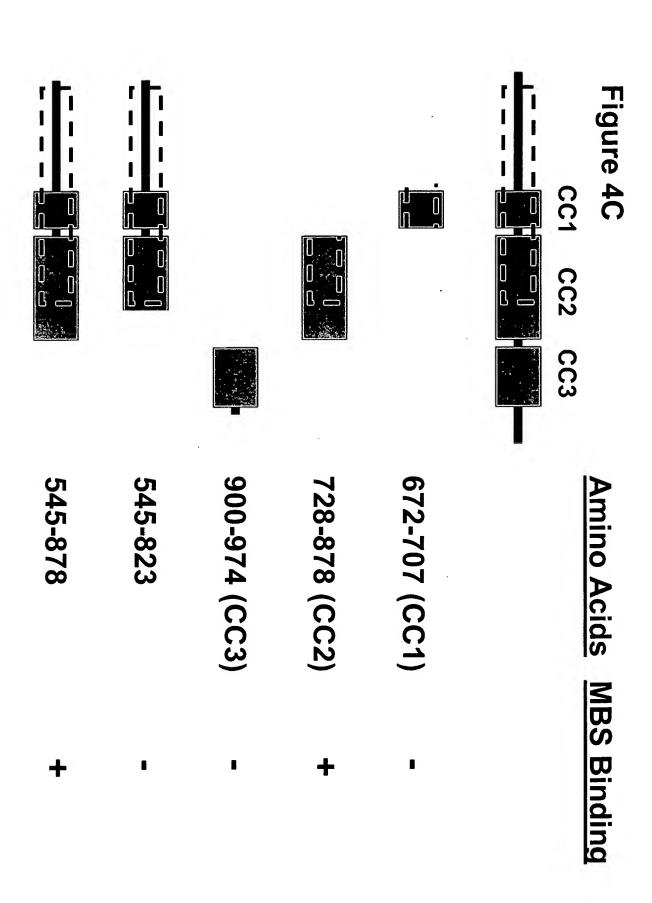
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Applicant(s): Michael E. Mendelsohn et al.

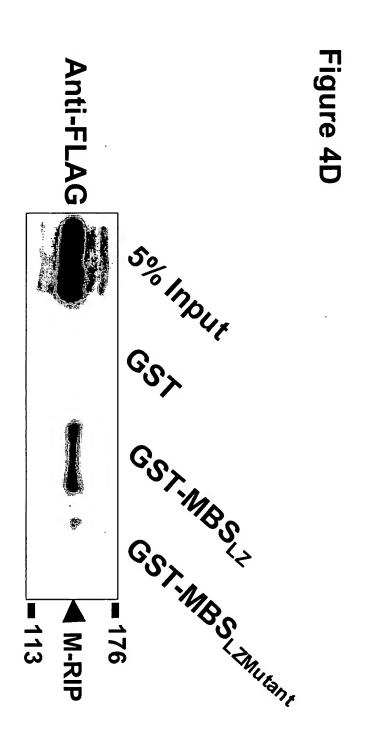
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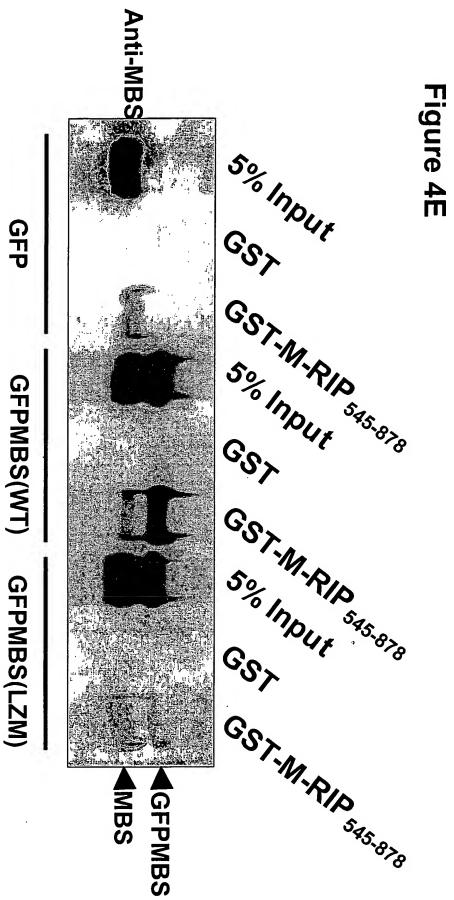
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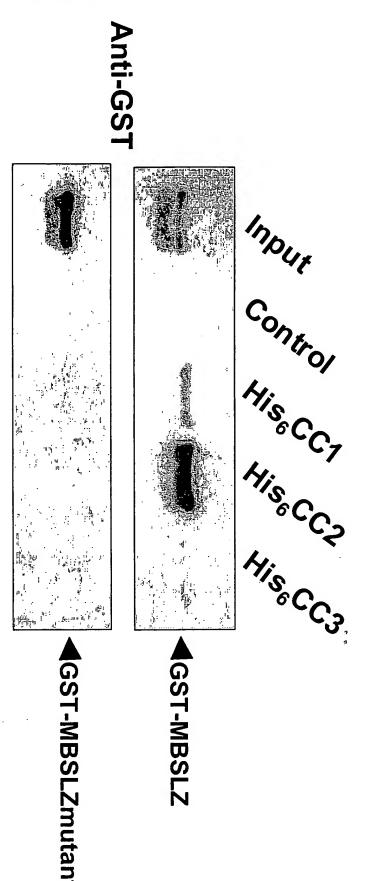


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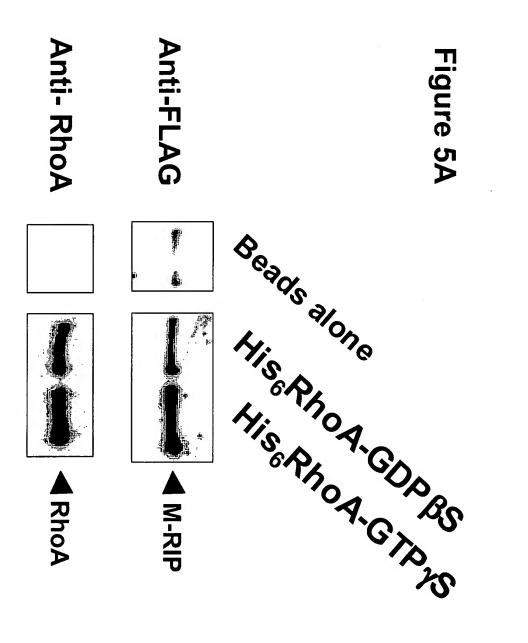


rigure 4F

Title: Compositions Involving M-RIP, and Related Methods for Screening for Anti-Hypertensive Agents and Uses Thereof

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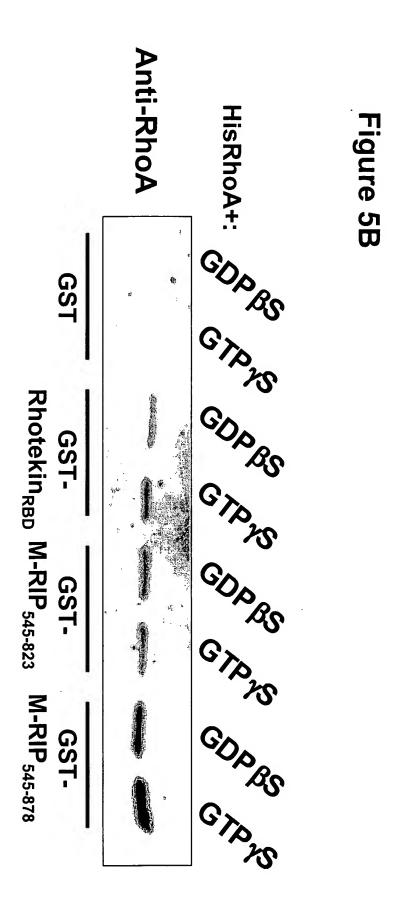
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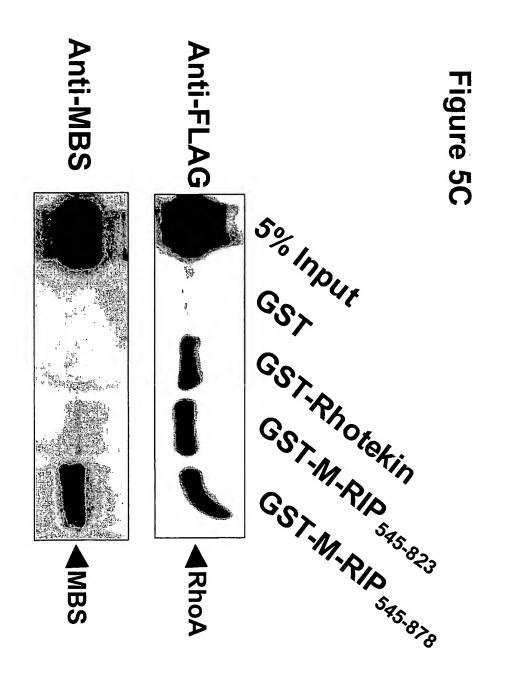


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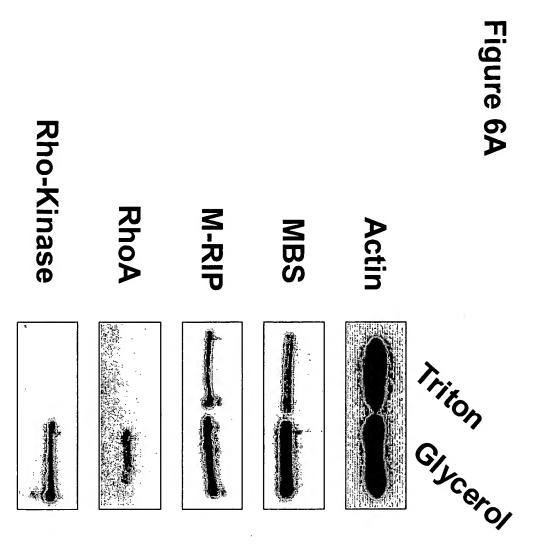
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Phalloidin

M-RIP

Figure 6B, top

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Phalloidin



Figure 6B, middle

Title: Compositions Involving M-RIP, and Related Methods for Screening for Anti-Hypertensive Agents and Uses Thereof

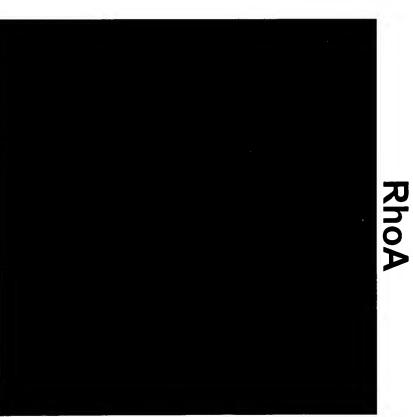
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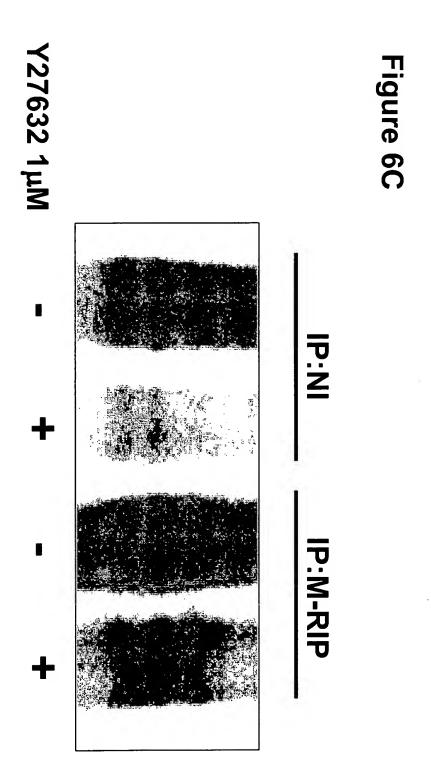
Figure 6B, bottom



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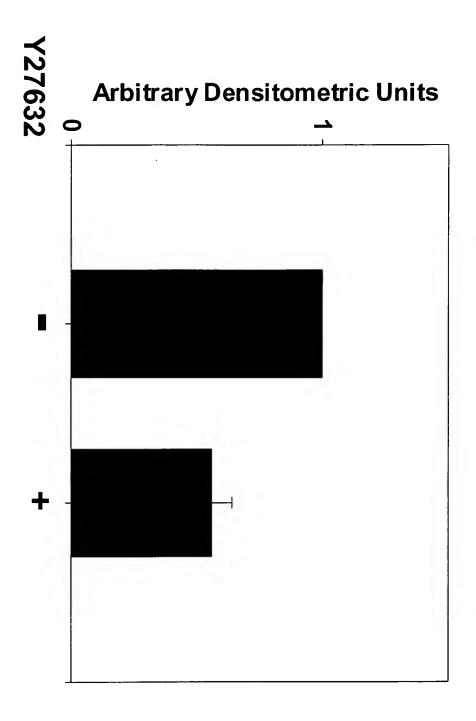


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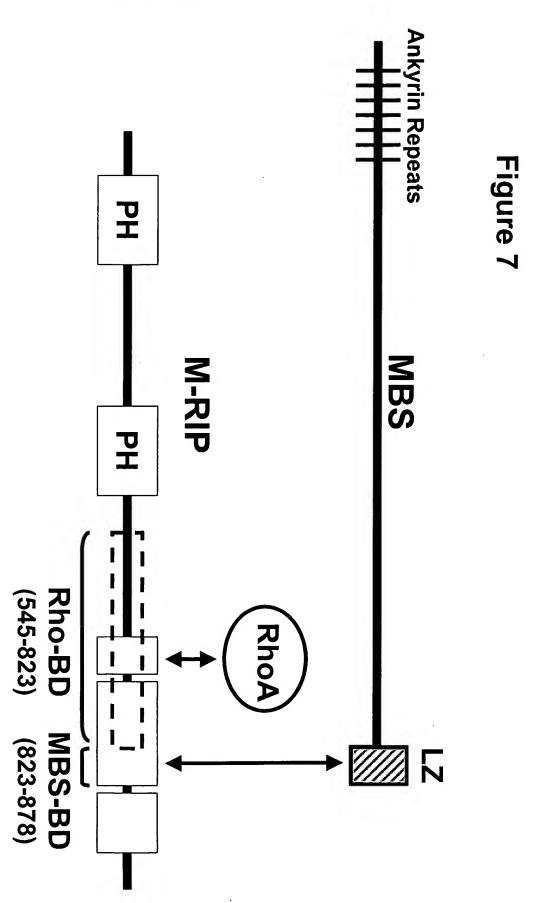


### Figure 6D

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